## SEQUENCE LISTING

<110> Curtis, Rory A.J. et al. <120> NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR <130> MNI-074CP2 <140> <141> <150> 09/431,367 <151> 01-11-1999 <150> US 09/259,951 <151> 01-03-1999 <160> 12 <170> PatentIn Ver. 2.0 <210> 1 <211> 3452 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (10)..(1506) <400> 1 tegggagee atg gtg gae egg gge eet etg etc acc teg gee atc atc tte 51Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe tac ctg gcc atc ggg gcg gcg atc ttc gaa gtg ctg gag gag cca cac Tyr Leu Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His 20 15 tgg aag gag gcc aag aaa aac tac tac aca cag aag ctg cat ctg ctc Trp Lys Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu aag gag ttc ccg tgc ctg ggt cag gag ggc ctg gac aag atc cta gag 195 Lys Glu Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu 50 243 gtg gta tct gat gct gca gga cag ggt gtg gcc atc aca ggg aac cag Val Val Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln 65 acc ttc aac aac tqg aac tgg ccc aat gca atg att ttt gca gcg acc 291 Thr Phe Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr 80 85 gtc att acc acc att gga tat ggc aat gtg gct ccc aag acc ccc gcc 339 Val Ile Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala

95

100

ggt cgc Gly Arg														387
ctg acg Leu Thr	tgg at Trp Il 13	.e Ser	gcc Ala	ctg Leu	ggc Gly	aag Lys 135	ttc Phe	ttc Phe	GJ À ààà	gga Gly	cgt Arg 140	gcc Ala	aag Lys	435
aga cta Arg Leu														483
cag atc Gln Ile 160														531
ctg gtg Leu Val 175														579
atc gag Ile Glu														627
ggt gac Gly Asp	ttt gt Phe Va 21	al Ala	ggt Gly	gtg Val	aac Asn	ccc Pro 215	agc Ser	gcc Ala	aac Asn	tac Tyr	cac His 220	gcc Ala	ctg Leu	675
tac cgc Tyr Arg														723
tcc ctt Ser Leu 240	ttt gt Phe Va	c aac al Asn	Trp	aag Lys 245	gtg Val	agc Ser	atg Met	ttt Phe	gtg Val 250	gaa Glu	gtc Val	cac His	aaa Lys	771
gcc att Ala Ile 255	aag aa Lys Ly	ag cgg ys Arg	cgg Arg 260	cgg Arg	cga Arg	cgg Arg	aag Lys	gag Glu 265	tcc Ser	ttt Phe	gag Glu	agc Ser	tcc Ser 270	819
cca cac Pro His	tcc cg Ser Ar	gg aag cg Lys 275	gcc Ala	ctg Leu	cag Gln	gtg Val	aag Lys 280	Gly aga	agc Ser	aca Thr	gcc Ala	tcc Ser 285	aag Lys	867
gac gtc Asp Val		le Phe												915
gac ctc Asp Leu	atc aa Ile Ly 305	ag cag ys Gln	atc Ile	ggg Gly	aag Lys 310	aag Lys	gcc Ala	atg Met	aag Lys	aca Thr 315	agc Ser	gly ggg	ggt Gly	963
ggg gag Gly Glu 320	acg gg Thr Gl	gc ccg Ly Pro	ggc Gly	cca Pro 325	ggg Gly	ctg Leu	ggg ggg	cct Pro	caa Gln 330	ggc Gly	ggt Gly	ggg Gly	ctc Leu	1011
cca gca Pro Ala 335														1059

														aaa Lys 365		1107
cac His	gta Val	tca Ser	agg Arg 370	tcc Ser	cca Pro	gat Asp	gag Glu	gag Glu 375	gct Ala	gtg Val	gca Ala	cgg Arg	gcc Ala 380	cct Pro	gaa Glu	1155
			Pro											cgc Arg		1203
														ctc Leu		1251
ttc Phe 415	cag Gln	gac Asp	gcc Ala	agc Ser	atc Ile 420	acc Thr	ttc Phe	gtg Val	aac Asn	acg Thr 425	gag Glu	gct Ala	ggc Gly	ctc Leu	tca Ser 430	1299
gac Asp	gag Glu	gag Glu	acc Thr	tcc Ser 435	aag Lys	tcc Ser	tcg Ser	cta Leu	gag Glu 440	gac Asp	aac Asn	ttg Leu	gca Ala	ggg Gly 445	gag Glu	1347
														atg Met		1395
														tct Ser		1443
														gct Ala		1491
			ggc Gly		tga	ggcaq	ggg (	ccgg	ctcc	cc ad	ccca	acctt	t tga	atggo	cctc	1546
ttc	cccc	ctc a	accct	tagg	gt gi	ccca	aagat	gad	ccgg	gacg	cct	ggcco	cct (	ggtg	gggggg	1606
cago	cata	gga a	actg	ggagt	g g	gggg	ccag	g ggd	cctt	ccta	acct	tcca	atc a	atcct	cagct	1666
agat	tgta	tgc (	ccgg	gaca	gg go	cctct	gtto	t tc	cagct	tgaa	ccat	cacco	ctg (	gctgt	ggggg	1726
cato	ctgt	cct (	gagct	ttgg	ct g	gtgta	atcto	c aca	aatgo	caaa	gaca	atgct	tgg (	ctggd	egggac	1786
aggt	tggg	cag (	gact	gacc	ct ga	agga	ggcct	t tg	cctgo	cagg	gtct	ttgt	ct o	cacca	atttgg	1846
tgga	agta	tca (	cacgo	gttc	c to	gaggt	ctg	g ggd	cctca	agct	gttt	aagt	ttt a	accg	gtatta	1906
ctga	agct	cgg (	catt	tgga	ga go	ggago	ctct	g aaq	gtgto	ctgg	gga	ggtad	ccg (	ctgt	gcgtgg	1966
ggt	cagg	tgt ·	ttcc	gtac	ca ca	agca	ggago	c ago	ggcct	tgcc	cgca	atcc	cag d	ctgt	gggcct	2026
gcc	ggtc	agg	tcgg	gcac	ct a	ctaca	aaaco	c gta	agtg	gggt	gga	ggct	gct	ggag	gtggga	2086
gtg	agga	gat	gagg	gcag	gg to	ctcaa	aacaq	g tc	ctgad	ctca	cag	ggcct	tgg a	aaaca	aagtcc	2146
tate	gtgg	gcc	tggg	gcct	gg g	gtcc	tcato	cto	cctt	gttg	gtct	tacto	cag (	gccca	agccca	2206

gagetgtgtt ccetgtetca ggtcaageag tggcagaege aaggetttet gtgggeecee 2266 aagtggtagg agggagagta gcagagcatg ggttactgga agccgggact gctagggctg 2326 gtggccaggg agctgcaaga gtgaggctca gctctggctg gttctgccct tacccctcct 2386 gecegeetga gaactgeaca eeetgeeege tggeeeeagg acetgeacte ecaateetge 2446 tgtcttctcc ttccctgtgc cctgaacaag gacctcactg cccgccttcc cctcccacca 2506 gcccccttgg gccaggcagg gtgaggccaa attgctcttg gcccacaaat gggtgatggt 2566 cagatatgtg aatcaagctc ctttctctag ctagtgtttg atgtgcacgt gtgtgtgcac 2626 aqtqcgtqtq tqcacacqca cacctqtqca ctcqtqtqtq tttaagaaag gaaaggattt 2686 gggctgggga gcaaaagata atgtgaaact gttggtggac tctctggtga ggggtgggca 2746 gaacttgctg ctactagagt tcttgggttc tccatgatgt tcaccctggg gctggcccac 2806 tgtgtcctga atgtttttgt tattttttgt tttatttttt aaacaaactg ctgtttttat 2866 atacctggaa tctgttgttg gcttcagagc cagtggttaa agagcagggt cccaaggatt 2926 gggagateta gtgtetgeec teetgeeetg caacteaatt gggeettttt eggtgaeete 2986 atccaaggcc atgatgtcaa gggccatgtc cccaagcaga ggtggagaag gggacactga 3046 ggtgagcaaa agcaggaagg ggcatccact gcgggtgact ggaggccggg caggaagcaa 3106 gtcatcagag ccgctcagct ccgttcactc tctgccttct gccccactac tgtggggcag 3166 tggggccaga gcccacctcc ccaacatgtg aagacagtga tgggcacgtg cccacacccc 3226 cactteteta geogtttgea gaggeegeea eecageaggg geetgaaaag gageageete 3286 gtatttttct gtgaaatgtt ttaatgaacc atgttgttgc tggttgtcct ggcatcgcgc 3346 acactgtatg tacatactgg caacgatgtc aaatgtaatt tattttaaca tttttacaat 3406 3452 aaaacatgag gtggacaggc caaaaaaaaa aaaaaaaaa aaaaaa

<210> 2 <211> 499 <212> PRT <213> Homo sapiens

<400> 2
Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu
1 5 10 15

Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys 20 25 30

Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu 35 40 45

Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val 50 55 60

Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile 90 Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val 170 165 Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu 185 Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp 200 195 Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg 215 Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu 230 235 225 Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile 250 Lys Lys Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His 265 Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val 280 Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu 290 300 Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Glu Glu 310 Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Leu Pro Ala 330 Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val 360 Ser Arg Ser Pro Asp Glu Glu Ala Val Ala Arg Ala Pro Glu Asp Ser

375

Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu 390 Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln 405 Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu 425 Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser 470 Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro 490 485 Lys Gly Thr <210> 3 <211> 1497 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(1497) <400> 3 atg gtg gac cgg ggc cct ctg ctc acc tcg gcc atc atc ttc tac ctg 48 Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu qcc atc ggg gcg gcg atc ttc gaa gtg ctg gag gag cca cac tgg aag 96 Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys 20 gag gcc aag aaa aac tac tac aca cag aag ctg cat ctg ctc aag gag 144 Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu 192 ttc ccg tgc ctg ggt cag gag ggc ctg gac aag atc cta gag gtg gta Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val tct gat gct gca gga cag ggt gtg gcc atc aca ggg aac cag acc ttc 240 Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe 65 288 aac aac tgg aac tgg ccc aat gca atg att ttt gca gcg acc gtc att Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile 85

acc ac Thr Th	cc att hr Ile	gga Gly 100	tat Tyr	ggc Gly	aat Asn	gtg Val	gct Ala 105	ccc Pro	aag Lys	acc Thr	ccc Pro	gcc Ala 110	ggt Gly	cgc Arg	336
ctc tt Leu Pl	tc tgt he Cys 115	Val	ttc Phe	tat Tyr	ggt Gly	ctc Leu 120	ttc Phe	ggg Gly	gtg Val	ccg Pro	ctc Leu 125	tgc Cys	ctg Leu	acg Thr	384
-	tc agt le Ser 30	gcc Ala	ctg Leu	ggc Gly	aag Lys 135	ttc Phe	ttc Phe	Gly ggg	gga Gly	cgt Arg 140	gcc Ala	aag Lys	aga Arg	cta Leu	432
ggg ca Gly Gl 145	ag tto ln Phe	ctt Leu	acc Thr	aag Lys 150	aga Arg	ggt Gly	gtg Val	agt Ser	ctg Leu 155	cgg Arg	aag Lys	gcg Ala	cag Gln	atc Ile 160	480
	gc aca ys Thr														528
	ca ccc ro Pro														576
ggc ct Gly Le	tc tac eu Tyr 195	Tyr	tcc Ser	ttc Phe	atc Ile	acc Thr 200	atc Ile	tcc Ser	acc Thr	atc Ile	ggc Gly 205	ttc Phe	ggt Gly	gac Asp	624
Phe Va	tg gcc al Ala 10														672
	tc gto he Val														720
ttt gi	tc aac al Asr	tgg Trp	aag Lys 245	gtg Val	agc Ser	atg Met	ttt Phe	gtg Val 250	gaa Glu	gtc Val	cac His	aaa Lys	gcc Ala 255	att Ile	768
aag aa Lys L	ag cgg ys Arg	cgg Arg 260	cgg Arg	cga Arg	cgg Arg	aag Lys	gag Glu 265	tcc Ser	ttt Phe	gag Glu	agc Ser	tcc Ser 270	cca Pro	cac His	816
tcc co Ser A	gg aag rg Lys 275	Ala	ctg Leu	cag Gln	gtg Val	aag Lys 280	ggg Gly	agc Ser	aca Thr	gcc Ala	tcc Ser 285	aag Lys	gac Asp	gtc Val	864
Asn I	tc ttc le Phe 90														912
atc atc Ile L	ag caq ys Glr	g atc n Ile	ggg Gly	aag Lys 310	aag Lys	gcc Ala	atg Met	aag Lys	aca Thr 315	agc Ser	Gly	ggt Gly	ggg Gly	gag Glu 320	960
acg go Thr G	gc ccc ly Pro	g ggc	cca Pro 325	ggg Gly	ctg Leu	ggg Gly	cct Pro	caa Gln 330	ggc Gly	ggt Gly	ggg Gly	ctc Leu	cca Pro 335	gca Ala	1008

ctg ccc cct Leu Pro Pro				l Val							1056
ccc acc ttg Pro Thr Leu 355											1104.
tca agg tcc Ser Arg Ser 370					Arg						1152
tcc cct gcc Ser Pro Ala 385											1200
gaa tgc gag Glu Cys Glu	cca tgg Pro Trp 405	gac gcc Asp Ala	cag gad Gln Asp	tac Tyr 410	cac His	cca Pro	ctc Leu	atc Ile	ttc Phe 415	cag Gln	1248
gac gcc agc Asp Ala Ser	atc acc Ile Thr 420	ttc gtg Phe Val	aac acc Asn Th: 42	Glu	gct Ala	ggc Gly	ctc Leu	tca Ser 430	gac Asp	gag Glu	1296
gag acc tcc Glu Thr Ser 435											1344
ccc cag cag Pro Gln Gln 450											1392
ccc tcc tcc Pro Ser Ser 465											1440
gtg cct tac Val Pro Tyr											1488
aag ggc aca Lys Gly Thr											1497
<210> 4 <211> 1575 <212> DNA <213> Homo	sapiens										
<220> <221> CDS <222> (122)	(1117)										
<400> 4 caacgcgtcc	gccgggca	cc agcag	gcgtt to	gcgaga	agga	gata	cgaç	jet g	gaco	jcctgg	60
cccttccctc	ccaccggg	tc ctagt	ccacc g	etece	ggcg	ccgç	getec	ecc ç	gctct	cccgc	120
t atg tac c Met Tyr A 1				Ala Pi					al Ar		169

						gtg Val										217
						gtg Val										265
						ttc Phe 55										313
						cgc Arg										361
gtc Val	gtc Val	caa Gln	gca Ala	tac Tyr 85	aaa Lys	aac Asn	gga Gly	gcc Ala	agc Ser 90	ctc Leu	ctc Leu	agc Ser	aac Asn	acc Thr 95	acc Thr	409
agc Ser	atg Met	Gly ggg	cgc Arg 100	tgg Trp	gag Glu	ctc Leu	gtg Val	ggc Gly 105	tcc Ser	ttc Phe	ttc Phe	ttt Phe	tct Ser 110	gtg Val	tcc Ser	457
						tat Tyr										505
						ttc Phe 135										553
ctc Leu 145	gtg Val	gtg Val	ctc Leu	aac Asn	cga Arg 150	ctg Leu	Gly ggg	cat His	ctc Leu	atg Met 155	cag Gln	cag Gln	gga Gly	gta Val	aac Asn 160	601
cac His	tgg Trp	gcc Ala	agc Ser	agg Arg 165	ctg Leu	ggg Gly	ggc Gly	acc Thr	tgg Trp 170	cag Gln	gat Asp	cct Pro	gac Asp	aag Lys 175	gcg Ala	649
cgg Arg	tgg Trp	ctg Leu	gcg Ala 180	ggc Gly	tct Ser	ggc Gly	gcc Ala	ctc Leu 185	ctc Leu	tcg Ser	ggc Gly	ctc Leu	ctg Leu 190	ctc Leu	ttc Phe	697
						ctc Leu										745
						gcc Ala 215										793
						atg Met										841
						ctg Leu										889

gcc Ala	ttg Leu	atc Ile	atc Ile 260	aaa Lys	ctc Leu	atc Ile	ctc Leu	tcc Ser 265	cag Gln	ctg Leu	gag Glu	acg Thr	cca Pro 270	Gly ggg	agg Arg	937
gta Val	tgt Cys	tcc Ser 275	tgc Cys	tgc Cys	cac His	cac His	agc Ser 280	tct Ser	aag Lys	gaa Glu	gac Asp	ttc Phe 285	aag Lys	tcc Ser	caa Gln	985
agc Ser	tgg Trp 290	aga Arg	cag Gln	gga Gly	cct Pro	gac Asp 295	cgg Arg	gag Glu	cca Pro	gag Glu	tcc Ser 300	cac His	tcc Ser	cca Pro	cag Gln	1033
caa Gln 305	gga Gly	tgc Cys	tat Tyr	cca Pro	gag Glu 310	gga Gly	ccc Pro	atg Met	gga Gly	atc Ile 315	ata Ile	cag Gln	cat His	ctg Leu	gaa Glu 320	1081
				gct Ala 325								tagt	tata	act		1127 .:
ccat	tctt	tg q	gtcgt	tcgt	cc to	eggta	agcaa	a gad	ccct	tgat	ttta	aagct	tt q	gcaca	atgtcc	1187
acco	caaa	cta a	aagad	ctaca	at t	tcca	atcca	a cc	ctaga	aggc	tgg	gtgca	agc 1	tatat	gatta	1247
atto	ctgc	cca a	atago	ggtai	ta ca	agaga	acato	g tco	ctgg	gtga	cato	gggat	gt	gactt	tcggg	1307
tgto	gggg	gca (	gcat	gccct	tt ct	ccc	ccact	tc	cttac	cttt	agc	gggct	gc a	aatgo	ccgccg	1367
atat	gat	ggc 1	tggga	agcto	ct g	gcago	ccata	a cg	gcaco	catg	aagt	agc	ggc a	aatgt	ttgag	1427
cgg	cacaa	ata a	agata	aggaa	ag ag	gtct	ggato	c to	tgate	gatc	acaç	gagco	cat o	cctaa	acaaac	1487
gga	atato	cac (	ccga	cctc	ct ti	tatgi	tgaga	a ga	gaaat	taaa	cato	cttat	gt a	aaaat	acaaa	1547
aaaa	aaaa	aaa a	aaaa	aaaa	gg go	cggc	cgc									1575
•																

<210> 5 <211> 332 <212> PRT <213> Homo sapiens

<400> 5

Met Tyr Arg Pro Arg Ala Arg Ala Ala Pro Glu Gly Arg Val Arg Gly 1 5 10 15

Cys Ala Val Pro Gly Thr Val Leu Leu Leu Leu Ala Tyr Leu Ala Tyr 20 25 30

Leu Ala Leu Gly Thr Gly Val Phe Trp Thr Leu Glu Gly Arg Ala Ala 35 40 45

Gln Asp Ser Ser Arg Ser Phe Gln Arg Asp Lys Trp Glu Leu Leu Gln 50 55 60

Asn Phe Thr Cys Leu Asp Arg Pro Ala Leu Asp Ser Leu Ile Arg Asp 65 70 75 80

Val Val Gln Ala Tyr Lys Asn Gly Ala Ser Leu Leu Ser Asn Thr Thr 85 90 95 Ser Met Gly Arg Trp Glu Leu Val Gly Ser Phe Phe Ser Val Ser 105 Thr Ile Thr Thr Ile Gly Tyr Gly Asn Leu Ser Pro Asn Thr Met Ala Ala Arg Leu Phe Cys Ile Phe Phe Ala Leu Val Gly Ile Pro Leu Asn Leu Val Val Leu Asn Arg Leu Gly His Leu Met Gln Gln Gly Val Asn 150 145 His Trp Ala Ser Arg Leu Gly Gly Thr Trp Gln Asp Pro Asp Lys Ala 170 Arg Trp Leu Ala Gly Ser Gly Ala Leu Leu Ser Gly Leu Leu Phe 180 Leu Leu Pro Pro Leu Leu Phe Ser His Met Glu Gly Trp Ser Tyr 200 Thr Glu Gly Phe Tyr Phe Ala Phe Ile Thr Leu Ser Thr Val Gly Phe Gly Asp Tyr Val Ile Gly Met Asn Pro Ser Gln Arg Tyr Pro Leu Trp 230 235 Tyr Lys Asn Met Val Ser Leu Trp Ile Leu Phe Gly Met Ala Trp Leu 250 Ala Leu Ile Ile Lys Leu Ile Leu Ser Gln Leu Glu Thr Pro Gly Arg Val Cys Ser Cys Cys His His Ser Ser Lys Glu Asp Phe Lys Ser Gln 280 Ser Trp Arg Gln Gly Pro Asp Arg Glu Pro Glu Ser His Ser Pro Gln Gln Gly Cys Tyr Pro Glu Gly Pro Met Gly Ile Ile Gln His Leu Glu 315 Pro Ser Ala His Ala Ala Gly Cys Gly Lys Asp Ser

Pro Ser Ala His Ala Ala Gly Cys Gly Lys Asp Ser 325 330

<210> 6 <211> 996 <212> DNA <213> Homo sapiens

<220> <221> CDS <222> (1)..(996)

<400>
atg tac cga ccg cga gcc cgg gcg gct ccc gag ggc agg gtc cgg ggc 48

Met Tyr Arg Pro Arg Ala Arg Ala Ala Pro Glu Gly Arg Val Arg Gly

1 5 10 15

tgc Cys	gcg Ala	gtg Val	ccc Pro 20	ggc Gly	acc Thr	gtg Val	ctc Leu	ctg Leu 25	ctg Leu	ctc Leu	gcc Ala	tac Tyr	ctg Leu 30	gct Ala	tac Tyr	96
ctg Leu	gcg Ala	ctg Leu 35	ggc Gly	acc Thr	ggc Gly	gtg Val	ttc Phe 40	tgg Trp	acg Thr	ctg Leu	gag Glu	ggc Gly 45	cgc Arg	gcg Ala	gcg Ala	144
					agc Ser											192
					gac Asp 70											240
					aaa Lys											288
					gag Glu											336
					ggc Gly											384
_	_			_	atc Ile			_								432
					cga Arg 150											480
					ctg Leu											528
					tct Ser											576
					ctg Leu											624
					ttc Phe											672
					gga Gly 230											720
					tcc Ser											768

260 265	cca ggg agg 816 Pro Gly Arg 270
gta tgt tcc tgc tgc cac cac agc tct aag gaa gac ttc Val Cys Ser Cys Cys His His Ser Ser Lys Glu Asp Phe 275 280 285	aag tcc caa 864 Lys Ser Gln
agc tgg aga cag gga cct gac cgg gag cca gag tcc cac Ser Trp Arg Gln Gly Pro Asp Arg Glu Pro Glu Ser His 290 295 300	tcc cca cag 912 Ser Pro Gln
caa gga tgc tat cca gag gga ccc atg gga atc ata cag Gln Gly Cys Tyr Pro Glu Gly Pro Met Gly Ile Ile Gln 305 310 315	cat ctg gaa 960 His Leu Glu 320
cct tct gct cac gct gca ggc tgt ggc aag gac agc Pro Ser Ala His Ala Ala Gly Cys Gly Lys Asp Ser 325 330	996
<210> 7 <211> 2287 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (136)(1074)	
<400> 7 taaaagctgc ggaattctaa tatcactcac tatagggagt cgacccac	gc gtccgggaac 60
taaaagctgc ggaattctaa tatcactcac tatagggagt cgacccac	eag ggctcgcggg 120
taaaagctgc ggaattctaa tatcactcac tatagggagt cgacccac taggtgccag acggtccgga ggcgggggcc acgtcagcgg ggccaccc gtcccggtgg gtgcc atg cgg agg ggc gcg ctt ctg gcg ggc Met Arg Arg Gly Ala Leu Leu Ala Gly	ag ggctcgcggg 120 gcc ttg gcc 171 Ala Leu Ala 10 gcg cgg ctg 219
taaaagctgc ggaattctaa tatcactcac tatagggagt cgacccac taggtgccag acggtccgga ggcgggggcc acgtcagcgg ggccaccc gtcccggtgg gtgcc atg cgg agg ggc gcg ctt ctg gcg ggc Met Arg Arg Gly Ala Leu Leu Ala Gly 1 5 gcg tac gcc gcg tac ctg gtg ctg ggc gcg ctg ttg gtg Ala Tyr Ala Ala Tyr Leu Val Leu Gly Ala Leu Leu Val	ag ggctcgcggg 120 gcc ttg gcc 171 Ala Leu Ala 10 gcg cgg ctg 219 Ala Arg Leu acg ctg cgg 267
taaaagctgc ggaattctaa tatcactcac tatagggagt cgacccac taggtgccag acggtccgga ggcggggcc acgtcagcgg ggccaccc gtcccggtgg gtgcc atg cgg agg ggc gcg ctt ctg gcg ggc Met Arg Arg Gly Ala Leu Leu Ala Gly 1 5  gcg tac gcc gcg tac ctg gtg ctg ggc gcg ctg ttg gtg Ala Tyr Ala Ala Tyr Leu Val Leu Gly Ala Leu Leu Val 15 20 25  gag ggg ccg cac gaa gcc agg ctc cga gcc gag ctg gag Glu Gly Pro His Glu Ala Arg Leu Arg Ala Glu Leu Glu	ag ggctcgcggg 120 gcc ttg gcc 171 Ala Leu Ala 10 gcg cgg ctg 219 Ala Arg Leu acg ctg cgg 267 Thr Leu Arg gcc ctg gac 315
tagatgccag acggtccgga ggcgggggcc acgtcagcgg ggccaccc  gtcccggtgg gtgcc atg cgg agg ggc gcg ctt ctg gcg ggc  Met Arg Arg Gly Ala Leu Leu Ala Gly  1 5  gcg tac gcc gcg tac ctg gtg ctg ggc gcg ctg ttg gtg Ala Tyr Ala Ala Tyr Leu Val Leu Gly Ala Leu Leu Val  15 20 25  gag ggg ccg cac gaa gcc agg ctc cga gcc gag ctg gag Glu Gly Pro His Glu Ala Arg Leu Arg Ala Glu Leu Glu  30 35 40  gcg cag ctg ctt cag cgc agc ccg tgt gtg gcc ccc Ala Gln Leu Gln Arg Ser Pro Cys Val Ala Ala Pro	ag ggctcgcggg 120 gcc ttg gcc 171 Ala Leu Ala 10 gcg cgg ctg 219 Ala Arg Leu acg ctg cgg 267 Thr Leu Arg gcc ctg gac 315 Ala Leu Asp 60 cgg gtc gtg 363

					ttc Phe											459
					cca Pro											507
					ggc Gly 130											555
					tca Ser											603
ctg Leu	agc Ser	atg Met	cgt Arg 160	tgg Trp	ggc Gly	tgg Trp	gac Asp	ccc Pro 165	cgg Arg	cgg Arg	gcg Ala	gcc Ala	tgc Cys 170	tgg Trp	cac His	651
					Gly ggg											699
					cac His											747
					atc Ile 210											795
					cct Pro											843
					ctc Leu											891
ctg Leu	cag Gln	acc Thr 255	ttc Phe	cgc Arg	cac His	gtg Val	tcc Ser 260	gac Asp	ctc Leu	cac His	ggc Gly	ctc Leu 265	acg Thr	gag Glu	ctc Leu	939
					ccg Pro											987
					ctg Leu 290											1035
	-	-			acc Thr	_							tago	etgg	ggc	1084
agco	ctctq	gcc a	aggct	tgg	gt gt	gcct	ggc	t t g	ggact	gag	gggt	ccaç	ggc d	gacca	agagct	1144
ggct	gtad	cag o	gaat	gtcca	ac ga	agcad	cagca	a ggt	gato	cttg	aggo	cctt	gee (	gtcca	accgtc	1204
tct	ccttt	tgt 1	ttcc	cagca	at ct	ggct	ggga	a tgt	gaaq	gggc	agca	actco	ct ç	gtccc	ccatgt	1264

cccqqqctcc actqqqcacc aacataacct tgttctctgt cctttctctc atcctcttta 1324 cactgtgtct ctctggctct ctggcattct cgctgcctct gtctttccct cttgctgtct 1384 ctgqttctca ttctctttca tqttccqkct gkgtctctca attaaccact cgtcaactgc 1444 tgattctact gggctgtggg ctcagacctc atttcaggca ccagattggt cgctacaccc 1504 tggacaagtg actgcccgtc tctgagcctt gatttcctca gctgccaaat gggaagaata 1564 qaaqaatttq cccctaaacc cctcctqtqt qctggccctg tgctagacag tgctggagac 1624 ataqttgggg gtggagaact gcccttatgg agcttgcagt ccagtgaggt ggacagacct 1684 gtccccagac agtgatggcc caaaatggtc aggactttaa tggaggargt gaaggtgttg 1744 aaagcacagg cagagtgggt caggkcttga agtcgkagaa gcatargggv ctaggcccaa 1804. tccangcctg gaaaagtmmg ggagngacnt tcctagagga acgggacatc gaactaaaga 1864 cctgaancta tgagaaatag gcaggaagaa gttgtaccnt gactcatttt tttcaggtgt 1924 ctccagggag caggacccat ggagggaccc ctggtgtagg chtggccaga tagactcttc 1984 actcaqcaqc ctggcaggca ggaarcagwc ataggmcccc agcccagaty tgaatggcmy 2044 sqqaqqtqct qcccttwccc rtqacaccat tgwaagwgct gyccacatwt gtatgktgtg 2104 ccctggaant cagccaggtt gagctcaaat cccaacttag ccasgtctgg cctgtgtcct 2164 tgggcagtca cactacctct ctgattttgt ttcmwwaatc atgtaaaatg gtgatcatca 2224 2287 agt

<210> 8 <211> 313 <212> PRT

<213> Homo sapiens

<400> 8

Met Arg Arg Gly Ala Leu Leu Ala Gly Ala Leu Ala Ala Tyr Ala Ala 1 5 10 15

Tyr Leu Val Leu Gly Ala Leu Leu Val Ala Arg Leu Glu Gly Pro His 20 25 30

Glu Ala Arg Leu Arg Ala Glu Leu Glu Thr Leu Arg Ala Gln Leu Leu 35 40 45

Gln Arg Ser Pro Cys Val Ala Ala Pro Ala Leu Asp Ala Phe Val Glu 50 55 60

Arg Val Leu Ala Ala Gly Arg Leu Gly Arg Val Val Leu Ala Asn Ala 65 70 75 80

Ser Gly Ser Ala Asn Ala Ser Asp Pro Ala Trp Asp Phe Ala Ser Ala

Leu Phe Phe Ala Ser Thr Leu Ile Thr Thr Val Gly Tyr Gly Tyr Thr 100 105 Thr Pro Leu Thr Asp Ala Gly Lys Ala Phe Ser Ile Ala Phe Ala Leu 120 Leu Gly Val Pro Thr Thr Met Leu Leu Leu Thr Ala Ser Ala Gln Arg 135 130 Leu Ser Leu Leu Thr His Val Pro Leu Ser Trp Leu Ser Met Arg 150 155 Trp Gly Trp Asp Pro Arg Arg Ala Ala Cys Trp His Leu Val Ala Leu Leu Gly Val Val Thr Val Cys Phe Leu Val Pro Ala Val Ile Phe Ala His Leu Glu Glu Ala Trp Ser Phe Leu Asp Ala Phe Tyr Phe Cys Phe Ile Ser Leu Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Ala Pro Gly Gln Pro Tyr Arg Ala Leu Tyr Lys Val Leu Val Thr Val 230 235 Tyr Leu Phe Leu Gly Leu Val Ala Met Val Leu Val Leu Gln Thr Phe 250 Arg His Val Ser Asp Leu His Gly Leu Thr Glu Leu Ile Leu Leu Pro 260 Pro Pro Cys Pro Ala Ser Phe Asn Ala Asp Glu Asp Asp Arg Val Asp 280 Ile Leu Gly Pro Gln Pro Glu Ser His Gln Gln Leu Ser Ala Ser Ser 290 295 His Thr Asp Tyr Ala Ser Ile Pro Arg 310 305 <210> 9 <211> 939 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(939) atg egg agg gge geg ett etg geg gge gee ttg gee geg tae gee geg 48 Met Arg Arg Gly Ala Leu Leu Ala Gly Ala Leu Ala Ala Tyr Ala Ala tac ctg gtg ctg gcg ctg ttg gtg gcg cgg ctg gag ggg ccg cac Tyr Leu Val Leu Gly Ala Leu Leu Val Ala Arg Leu Glu Gly Pro His 30

٠.:

		agg Arg 35											144
-	_	agc Ser	_	_	 _	-	-	_	 -			-	192
		ctg Leu											240
		tcc Ser											288
		ttc Phe											336
		ctg Leu 115											384
		gtg Val											432
		ctg Leu											480
		tgg Trp											528
		gtc Val											576
		ctc Leu 195											624
		tct Ser											672
-		ggc Gly	-			_		_	 -	_		_	720
		ttc Phe											768
_		gtg Val		_			_			_	_		816

	ccg Pro															864
	ctg Leu 290															912
	acc Thr															939
<21: <21: <21: <22: <22:	0> 10 1> 10 2> D0 3> H0 0> 1> C0 2> (0)	506 NA omo :	_													
	0> 10 ggga	-	egeca	atct	ga gt	agtt	cgga	a aga	aacto	gaac	atga	atga	gtt (	gccg	gctgct	60
tcc	tgag	tcc 1	ttgg	ggaag	gc ac	cacgo	cacca	a tco	cacti	tagc	acto	ggag	cct (	ggct	gttctc	120
cgg	gcac	cc t	tacco	ccato	ct to	ectg	gegg	g gct	tag			_		ctt Leu 5		174
	gct Ala															222
	ccc Pro															270
	ggc Gly 40		_			_		_				_	_			318
	gtg Val															366
	gat Asp															414
	tgc Cys															462
	ctg Leu															510
	ttc Phe 120															558

					tac Tyr 140										606
					ttt Phe										654
_			_		ctg Leu	_									702
					ttc Phe										750
					aag Lys										798 
-	_		_		atc Ile 220		_	-	_						846
					tca Ser										894
_					gag Glu		_			_	_				942
					aac Asn										990
					agc Ser		_	_	_	_	 -	_			1038
					ctc Leu 300										1086
		_	_	_	gcc Ala							_	_	-	1134
					tat Tyr										1182
		_		-	tta Leu										1230
				_	gga Gly	_					_		_	_	1278

gtg caa aac agg ctg att gac ata tac aaa aat gtt atg cta ttc ttt 1326 Val Gln Asn Arg Leu Ile Asp Ile Tyr Lys Asn Val Met Leu Phe Phe 375 380 385 gca aaa ggg aag ttt tac cac ctt gtt aaa aag tgaaggtttc attatctctc 1379 Ala Lys Gly Lys Phe Tyr His Leu Val Lys Lys 395 aggtgacaga cactggctga gctggttttc ttgtgttgtc tttcagggtc atgcagcctg 1439 tcacctgaga ccttcagtct tggagacaaa tcccttatga gagccaagtt cagtcttgag 1499 gccctgc 1506 <210> 11 <211> 401 <212> PRT <213> Homo sapiens --: <400> 11 Met Leu Pro Leu Pro Pro Ala Pro Leu Ala Leu His Ala Ser Gly Thr Met Glu Val Ser Gly His Pro Gln Ala Arg Arg Cys Cys Pro Glu Ala Leu Gly Lys Leu Phe Pro Gly Leu Cys Phe Leu Cys Phe Leu Val Thr Tyr Ala Leu Val Gly Ala Val Val Phe Ser Ala Ile Glu Asp Gly Gln Val Leu Val Ala Ala Asp Asp Gly Glu Phe Glu Lys Phe Leu Glu 75 Glu Leu Cys Arg Ile Leu Asn Cys Ser Glu Thr Val Val Glu Asp Arg Lys Gln Asp Leu Gln Gly His Leu Gln Lys Val Lys Pro Gln Trp Phe 105 Asn Arg Thr Thr His Trp Ser Phe Leu Ser Ser Leu Phe Phe Cys Cys Thr Val Phe Ser Thr Val Gly Tyr Gly Tyr Ile Tyr Pro Val Thr Arg Leu Gly Lys Tyr Leu Cys Met Leu Tyr Ala Leu Phe Gly Ile Pro Leu Met Phe Leu Val Leu Thr Asp Thr Gly Asp Ile Leu Ala Thr Ile Leu Ser Thr Ser Tyr Asn Arg Phe Arg Lys Phe Pro Phe Thr Arg Pro 180 Leu Leu Ser Lys Trp Cys Pro Lys Ser Leu Phe Lys Lys Pro Asp 200

Pro Lys Pro Ala Asp Glu Ala Val Pro Gln Ile Ile Ser Ala Glu

220

215

210

Glu Le	ı Pro	Gly	Pro	Lys 230	Leu	Gly	Thr	Cys	Pro 235	Ser	Arg	Pro	Ser	Cys 240	
Ser Me	c Glu	Leu	Phe 245	Glu	Arg	Ser	His	Ala 250	Leu	Glu	Lys	Gln	Asn 255	Thr	
Leu Gl	n Leu	Pro 260	Pro	Gln	Ala	Met	Glu 265	Arg	Ser	Asn	Ser	Cys 270	Pro	Glu	•
Leu Va	L Leu 275		Arg	Leu	Ser	Tyr 280	Ser	Ile	Ile	Ser	Asn 285	Leu	Asp	Glu	
Val Gly 29		Gln	Val	Glu	Arg 295	Leu	Asp	Ile	Pro	Leu 300	Pro	Ile	Ile	Ala	
Leu Ile 305	e Val	Phe	Ala	Tyr 310	Ile	Ser	Суѕ	Ala	Ala 315	Ala	Ile	Leu	Pro	Phe 320	
Trp Gli	ı Thr	Gln	Leu 325	Asp	Phe	Glu	Asn	Ala 330	Phe	Tyr	Phe	Суѕ	Phe 335	Val	
Thr Le	ı Thr	Thr 340	Ile	Gly	Phe	Gly	Asp 345	Thr	Val	Leu	Glu	His 350	Pro	Asn	
Phe Phe	Leu 355	Phe	Phe	Ser	Ile	Tyr 360	Ile	Ile	Val	Gly	Met 365	Glu	Ile	Val	
Phe Ile 370		Phe	Lys	Leu	Val 375	Gln	Asn	Arg	Leu	Ile 380	Asp	Ile	Tyr	Lys	
Asn Val	. Met	Leu	Phe	Phe 390	Ala	Lys	Gly	Lys	Phe 395	Tyr	His	Leu	Val	Lys 400	
Lys											•				
<210> 12 <211> 1203 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)(1203)															
<400> 1	2														
atg cto Met Leu	ctg					_			-	_		_			48
acg ato															96
gcc cto Ala Lei															144
acc tac Thr Tyr 50	Ala														192

							gat Asp								240
		-	_		_		tgc Cys	-	_			_	-	_	288
							ctg Leu								336
							ttc Phe 120								384
_			_				tat Tyr					_			432
							ctc Leu								480
_			_		_	_	aca Thr		_	_	_				528
							cga Arg						_		576
			_		_		aaa Lys 200			_			_	_	624
	_		_	_	_	_	gtc Val		_			_	-	-	672
							ggc Gly								720
							tct Ser								768
							atg Met								816
_		_		_			tac Tyr 280			_		_	-	-	864
							ttg Leu								912

				tac Tyr 310							960
				gat Asp							1008
				Gly ggg							1056
		_		tcc Ser				_	 _		 1104
				ttg Leu							1152
	-	-		ttt Phe 390	-		_			-	1200
aag Lys											1203